

Figure 1/1  
SEQ ID No.: 1

## DNA sequence:

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1  ATGAGGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGCG ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCAAGCCCT GAAGGGCCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCCTGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCCTCC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCG ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCCTATGAC AACTACGTCA CCATCCTTGA
951 TGAAGAAACA CTGAAAGCGT GGATTGCGAA GCTGGAAAAA GCGCCGGTAT
1001 TTGCATTTGA TACCGAAACC GACAGCCTTG ATAACATCTC TGCTAACCTG
1051 GTCGGGCTTT CTTTTGCTAT CGAGCCAGGC GTAGCGGCAT ATATTCCGGT
1101 TGCTCATGAT TATCTTGATG CGCCCGATCA AATCTCTCGC GAGCGTGCAC
1151 TCGAGTTGCT AAAACCGCTG CTGGAAGATG AAAAGGCGCT GAAGGTCGGG
1201 CAAAACCTGA AATACGATCG CGGTATTCTG GCGAACTACG GCATTGAACT
1251 GCGTGGGATT GCGTTTGATA CCATGCTGGA GTCCTACATT CTCAATAGCG
1301 TTGCCGGGCG TCACGATATG GACAGCCTCG CGGAACGTTG GTTGAAGCAC
1351 AAAACCATCA CTTTTGAAGA GATTGCTGGT AAAGGCAAAA ATCAACTGAC
1401 CTTTAACCAG ATTGCCCTCG AAGAAGCCGG ACGTTACGCC GCCGAAGATG
1451 CAGATGTCAC CTTGCAGTTG CATCTGAAAA TGTGGCCGGA TCTGCAAAAA
1501 CACGAGAGGC TCCTTTGGCT TTACCGGGAG GTGGAGAGGC CCCTTTCCGC
1551 TGTCTTGGCC CACATGGAGG CCACGGGGGT GCGCCTGGAC GTGGCCTATC
1601 TCAGGGCCTT GTCCCTGGAG GTGGCCGAGG AGGTCGCCCC CCTCGAGGCC
1651 GAGGTCTTCC GCCTGGCCGG CCACCCCTTC AACCTCAACT CCCGGGACCA
1701 GCTGGAAAGG GTCCTCTTTG ACGAGCTAGG GCTTCCCGCC ATCGGCAAGA
1751 CGGAGAAGAC CGGCAAGCGC TCCACCAGCG CCGCCGTCCT GGAGGCCCTC
1801 CGCGAGGCCC ACCCATCGT GGAGAAGATC CTGCAGTACC GGGAGCTCAC
1851 CAAGCTGAAG AGCACCTACA TTGACCCCTT GCCGGACCTC ATCCACCCCA
1901 GGACGGGCCG CCTCCACACC CGCTTCAACC AGACGGCCAC GGCCACGGGC
1951 AGGCTAAGTA GCTCCGATCC CAACCTCCAG AACATCCCCG TCCGCACCCC
2001 GCTTGGGCAG AGGATCCGCC GGGCCTTCAT CGCCGAGGAG GGGTGGCTAT
2051 TGGTGGCCCT GGACTATAGC CAGATAGAGC TCAGGGTGCT GGCCACCTC
2101 TCCGGCGACG AGAACCTGAT CCGGTCTTTC CAGGAGGGGC GGGACATCCA
2151 CACGGAGACC GCCAGCTGGA TGTTGCGCGT CCCCCGGGAG GCCGTGGACC
2201 CCCTGATGCG CCGGGCGGCC AAGACCATCA ACTTCGGGGT CCTCTACGGC
2251 ATGTCGGCCC ACCGCCTCTC CCAGGAGCTA GCCATCCCTT ACGAGGAGGC
2301 CCAGGCCTTC ATTGAGCGCT ACTTTCAGAG CTTCCCCAAG GTGCGGGCCT
2351 GGATTGAGAA GACCCTGGAG GAGGGCAGGA GGCGGGGGTA CGTGGAGACC
2401 CTCTTCGGCC GCCGCCGCTA CGTGCCAGAC CTAGAGGCCC GGGTGAAGAG
2451 CGTGCGGGAG GCGGCCGAGC GCATGGCCTT CAACATGCCC GTCCAGGGCA
2501 CCGCCGCCGA CCTCATGAAG CTGGCTATGG TGAAGCTCTT CCCCAGGCTG

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Figure 1/2  
SEQ ID No.: 1

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2551 GAGGAAATGG GGGCCAGGAT GCTCCTTCAG GTCCACGACG AGCTGGTCCT
2601 CGAGGCCCCA AAAGAGAGGG CGGAGGCCGT GGCCCGGCTG GCCAAGGAGG
2651 TCATGGAGGG GGTGTATCCC CTGGCCGTGC CCCTGGAGGT GGAGGTGGGG
2701 ATAGGGGAGG ACTGGCTCTC CGCCAAGGAG TGA

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SEQ ID No.: 7

amino acid sequence:

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1  MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51  TTSRGEPVQA VYGFAKSLLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLLSDMI HVLHPEGYLI TPWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGECT ARKLLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLH
301 EFGLLESPYD NYVTILDEET LKAWIAKLEK APVFAFDDET DSLDNISANL
351 VGLSFAIEPG VAAYIPVAHD YLDAPDQISR ERALELLKPL LEDEKALKVG
401 QNLKYDRGIL ANYGIELRGI AFDTMLESYI LNSVAGRHDH DSLAERWLKH
451 KTITFEEIAG KGKNQLTFNQ IALEEAGRYA AEDADVTLLQ HLKMWPDLOK
501 HERLLWLYRE VERPLSAVLA HMEATGVRLD VAYLRALSLE VAEVARLEA
551 EVFRLAGHPF NLNSRDQLER VLFDELGLPA IGKTEKTGKR STSAÄVLEAL
601 REAHPIVEKI LQYRELTKLK STYIDPLPDL IHPRTGRLHT RFNQATATATG
651 RLSSSDPNLQ NIPVRTPLGQ RIRRAFIAEE GWLLVALDYS QIELRVLAHL
701 SGDENLIRVF QEGRDIHTET ASWMFGVPRE AVDPLMRRAA KTINFGVLYG
751 MSAHRLSQEL AIPYEEAQAF IERYFQSFPK VRAWIEKTLE EGRRRGYVET
801 LFGRRRYVPD LEARVKSVRE AAERMAFNMP VQGTADLMK LAMVKLFPRL
851 EEMGARMLLQ VHDELVLLEP KERAFAVARL AKEVMEGVYP LAVPLEVEVG
901 IGEDWLSAKE

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Figure 2/1  
SEQ ID No.: 2

## DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCTGGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGTCTCTTTC
501 CGACCGCATC CACGTCTCTC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCG ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACGGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAG CCCCTATGAC AACTACGTCA CCATCCTTGA
951 TGAAGAAACA CTGAAAGCGT GGATTGCGAA GCTGGAAAAA GCGCCGGTAT
1001 TTGCATTTGA TACCGAAACC GACAGCCTTG ATAACATCTC TGCTAACCTG
1051 GTCGGGCTTT CTTTGTCTAT CGAGCCAGGC GTAGCGGCAT ATATTCCGGT
1101 TGCTCATGAT TATCTTGATG CGCCCGATCA AATCTCTCGC GAGCGTGCAC
1151 TCGAGTTGCT AAAACCGCTG CTGGAAGATG AAAAGGCGCT GAAGGTCGGG
1201 CAAAACCTGA AATACGATCG CGGTATTCTG GCGAACTACG GCATTGAACT
1251 GCGTGGGATT GCGTTTGATA CCATGCTGGA GTCCTACATT CTCAATAGCG
1301 TTGCCGGGCG TCACGATATG GACAGCCTCG CGGAACGTTG GTTGAAGCAC
1351 AAAACCATCA CTTTTGAAGA GATTGCTGGT AAAGGCAAAA ATCAACTGAC
1401 CTTTAAQAG ATTGCCCTCG AAGAAGCCGG ACGTTACGCC GCCGAAGATG
1451 CAGATGTQAC CTTGCAGTTG CATCTGAAAA TGTGGCCGGA TCTGCAAAAA
1501 CACAAAGGSC CGTTGAACGT CTTGAGAAAT ATCGAAATGC CGCTGGTGCC
1551 GGTGCTTTCA CGCATTGAAC GTAACGGTGT GCGCCTGGAC GTGGCCTATC
1601 TCAGGGCCTT GTCCTGGAG GTGGCCGAGG AGATCGCCCG CCTCGAGGCC
1651 GAGGTCTTCC GCCTGGCCGG CCACCCCTTC AACCTCAACT CCCGGGACCA
1701 GCTGGAAAGG GTCCTCTTTG ACGAGCTAGG GCTTCCCGCC ATCGGCAAGA
1751 CGGAGAAGAC CGGCAAGCGC TCCACCAGCG CCGCCGTCCT GGAGGCCCTC
1801 CGCGAGGCCC ACCCATCGT GGAGAAGATC CTGCAGTACC GGGAGCTCAC
1851 CAAGCTGAAG AGCACCTACA TTGACCCCTT GCCGGACCTC ATCCACCCCA
1901 GGACGGGCCG CCTCCACACC CGCTTCAACC AGACGGCCAC GGCCACGGGC
1951 AGGCTAAGTA GTCCTGATCC CAACCTCCAG AACATCCCCG TCCGCACCCC
2001 GCTTGGGCAG AGGATCCGCC GGGCCTTCAT CGCCGAGGAG GGGTGGCTAT
2051 TGGTGGCCCT GGAATATAGC CAGATAGAGC TCAGGGTGCT GGCCACCTC
2101 TCCGGCGACG AGAACCTGAT CCGGTCTTTC CAGGAGGGGC GGGACATCCA
2151 CACGGAGACC GCCAGCTGGA TGTTGCGCGT CCCCCGGGAG GCCGTGGACC
2201 CCCTGATGCG CCGGGCGGCC AAGACCATCA ACTTCGGGGT CCTCTACGGC
2251 ATGTCGGCCC ACCGCCTCTC CCAGGAGCTA GCCATCCCTT ACGAGGAGGC
2301 CCAGGCCTTC ATTGAGCGCT ACTTTCAGAG CTTCCTCAAG GTGCGGGCCT
2351 GGATTGAGAA GACCCTGGAG GAGGGCAGGA GGCGGGGGTA CGTGGAGACC
2401 CTCTTCGGCC GCCGCCGCTA CGTGCCAGAC CTAGAGGCCC GGGTGAAGAG
2451 CGTGCGGGAG GCGGCCGAGC GCATGGCCTT CAACATGCCC GTCCAGGGCA
2501 CCGCCGCCGA CCTCATGAAG CTGGCTATGG TGAAGCTCTT CCCCAGGCTG

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Figure 2/2  
SEQ ID No.: 2

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2551 GAGGAAATGG GGGCCAGGAT GCTCCTTCAG GTCCACGACG AGCTGGTCCCT
2601 CGAGGCCCCA AAAGAGAGGG CGGAGGCCGT GGCCCGGCTG GCCAAGGAGG
2651 TCATGGAGGG GGTGTATCCC CTGGCCGTGC CCCTGGAGGT GGAGGTGGGG
2701 ATAGGGGAGG ACTGGCTCTC CGCCAAGGAG TGA

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SEQ ID No.: 8

amino acid sequence:

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1  MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51  TTSRGEPVQA VYGFAXSLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRIILTADK DLYQLLSDRI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGECT ARKLLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH
301 EFGLLESPYD NYVTILDEET LKAWIAKLEK APVFAFDTET DSLDNISANL
351 VGLSFAIEPG VAAYIPVAHD YLDAPDQISR ERALELLKPL LEDEKALKVG
401 QNLKYDRGIL ANYGIELRGI AFDTMLESYI LNSVAGRHDM DSLAERWLKH
451 KTITFEEIAG KGKNQLTFNQ IALEEAGRYA AEDADVTLQL HLKMWPDLOK
501 HKGPLNVFEN IEMPLVPVLS RIERNGVRDL VAYLRALSLE VAEIARLEA
551 EVFRLAGHPF NLNSRDQLER VLFDELGLPA IGKTEKTGKR STSAAVLEAL
601 REAHPIVEKI LQYRELTKLK STYIDPLPDL IHPRTGRLHT RFNQATATATG
651 RLSSSDPNLQ NIPVRTPLGQ RIRRAFIAEE GWLLVALDYS QIELRVLAHL
701 SGDENLIRVF QEGRDIHTET ASWMFGVPRE AVDPLMRRAA KTFNFGVLYG
751 MSAHRLSQEL AIPYEEAQAF IERYFQSFPK VRAWIEKTLE EGRRRGYVET
801 LFGRRRYVPD LEARVKSURE AAERMAFNMP VQGTAADLMK LAMVKLFPRL
851 EEMGARMMLQ VHDELVLLEP KERAFAVARL AKEVMEGVYP LAVPLEVEVG
901 IGEDWLSAKE

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Figure 3/1  
SEQ ID No.: 3

DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGC ATGCTACCGC TATTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT FCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCTGGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCCTCC ACCCGGAGGG GTACCTCATC ACCCGGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCC ACCAGTGGGC GACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCCCCGTT GGATACAGAA TAGTGAAAGA
951 CCTGGTGAA TTTGAAAAAC TCATAGAGAA ACTGAGAGAA TCCCTTCGT
1001 TCGCCATAGA TCTTGAGACG TCTTCCCTCG ATCCTTTCGA CTGCGACATT
1051 GTCGGTATCT CTGTGTCTTT CAAACCAAAG GAAGCGTACT ACATACCACT
1101 CCATCATAGA AACGCCCAGA ACCTGGATGA AAAAGAAGTT CTGAAAAAGC
1151 TAAAAGAAAT CCTGGAGGAC CCCGGAGCAA AGATCGTTGG TCAGAATTTG
1201 AAATTCGATT ACAAGGTGTT GATGGTAAAG GGTGTTGAAC CTGTCCCTCC
1251 TCACTTCGAC ACGATGATAG CGGCTTACCT TCTTGAGCCG AACGAAAAGA
1301 AGTTCAATCT GGACGATCTC GCATTGAAAT TTCTTGATA CAAATGACC
1351 TCTTACCAGG AACTCATGTC CTTCTCTTCT CCGCTGTTTG GTTTCAGTTT
1401 TGCCGATGTT CTTGTAGAAA AAGCAGCGAA CTATTCCTGT GAAGATGCCG
1451 ACATCACCTA CAGACTCTAC AAGATCCTGA GCTTAAACT CCACGAGGAG
1501 AGGCTCCTTT GGCTTTACCG GGAGGTGGAG AGGCCCTTT CCGCTGTCCT
1551 GGCCACATG GAGGCCACGG GGTGCGCCT GGACGTGGCC TATCTCAGGG
1601 CCTTGTCCTT GGAGGTGGCC GAGGAGATCG CCCGCTCGA GGCAGAGGTC
1651 TTCCGCTGG CCGGCCACCC CTTCAACCTC AACTCCCGGG ACCAGCTGGA
1701 AAGGTCCTC TTTGACGAGC TAGGGCTTCC CGCCATCGGC AAGACGGAGA
1751 AGACCGCAA GCGCTCCACC AGCGCCGCCG TCCTGGAGGC CCTCCGCGAG
1801 GCCACCCCA TCGTGGAGAA GATCCTGCAG TACCGGAGC TCACCAAGCT
1851 GAAGAGACC TACATTGACC CCTTGCCGGA CCTCATCCAC CCCAGGACGG
1901 GCGCCTCCA CACCCGCTTC AACCAGACGG CCACGGCCAC GGGCAGGCTA
1951 AGTAGCTCCG ATCCCAACCT CCAGAACATC CCCGTCCGCA CCCCCTTGG
2001 GCAGAGGATC CGCCGGGCCT TCATCGCCGA GGAGGGGTGG CTATTGGTGG
2051 CCCTGGAATA TAGCCAGATA GAGCTCAGGG TGCTGGCCCA CCTCTCCGGC
2101 GACGAGAACC TGATCCGGGT CTTCCAGGAG GGGCGGGACA TCCACACGGA
2151 GACCGCCAGC TGGATGTTG GCGTCCCCG GGAGGCCGTG GACCCCTGA
2201 TGCGCCGGG GGCACAGACC ATCAACTTCG GGGTCCTCTA CGGCATGTCG
2251 GCCACCGCC TCTCCAGGA GCTAGCCATC CTTACGAGG AGGCCAGGC
2301 CTTCAATTGAG CGCTACTTTC AGAGCTTCCC CAAGGTGCGG GCCTGGATTG
2351 AGAAGACCCT GGAGGAGGGC AGGAGGCGGG GGTACGTGGA GACCTCTTC
2401 GGCCGCCGCC GCTACGTGCC AGACCTAGAG GCGCGGTGA AGAGCGTGG
2451 GGAGGCGGCC GAGCGCATGG CCTTCAACAT GCGCGTCCAG GGCACCGCCG
2501 CCGACCTCAT GAAGCTGGCT ATGGTGAAGC TCTTCCCCAG GCTGGAGGAA

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Figure 3/2  
SEQ ID No.: 3

2551 ATGGGGGCCA GGATGCTCCT TCAGGTCCAC GACGAGCTGG TCCTCGAGGC  
2601 CCCAAAAGAG AGGGCGGAGG CCGTGGCCCG GCTGGCCAAG GAGGTCATGG  
2651 AGGGGGTGTA TCCCCTGGCC GTGCCCTGG AGGTGGAGGT GGGGATAGGG  
2701 GAGGACTGGC TCTCCGCCAA GGAGTGA

SEQ ID No.: 9

amino acid sequence:

1 MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL  
51 TTSRGEVPQA VYGFAKSLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA  
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG  
151 YEVRILTADK DLYQLLSDRI HVLHPEGYLI TPWLWEKYG LRPDQWADYR  
201 ALTGDESDNL PGVKGIGECT ARKLEEWGS LEALLKNLDR LKPAIREKIL  
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH  
301 EFGLLESPPV GYRIVKDLVE FEKLIEKLRE SPSFAIDLET SSLDPFDCDI  
351 VGISVSFKPK EAYYIPLHHR NAQNLDEKEV LKKLKEILED PGAKIVGQNL  
401 KFDYKVLNVK GVEPVPPHFD TMIAAYLLEP NEKKFNLDL ALKFLGYKMT  
451 SYQELMSFSS PLFGFSFADV PVEKAANYSC EDADITYRLY KILSLKLHEE  
501 RLLWLYREVE RPLSAVLAHM EATGVRLDVA YLRALSLEVA EEIARLEAEV  
551 FRLAGHPFNL NSRDQLERVL FDELGLPAIG KTEKTGKRST SAAVLEALRE  
601 AHPIVEKILQ YRELTKLKST YIDPLPLIH PRTGRLHTRF NQTATATGRL  
651 SSSDPNLQNI PVRTPLGQRI RRAFIAEEGW LLVALDYSQI ELRVLAHLSG  
701 DENLIRVFQE GRDIHTETAS WMFGVPREAV DPLMRRAAKT INFGVLYGMS  
751 AHRLSQELAI PYEEAQAFIE RYFQSFPKVR AWIEKTLEEG RRRGYVETLF  
801 GRRRYVPDLE ARVKSUREAA ERMAFNMPVQ GTAADLMKLA MVKLFPRLEE  
851 MGARMLLQVH DELVLEAPKE RAEAVARLAK EVMEGVYPLA VPLEVEVGIG  
901 EDWLSAKE

Figure 4/1  
SEQ ID No.: 4

## DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51 AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCCTGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCTCTC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCC ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGCGAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCCCCGTT GGATACAGAA TAGTGAAAGA
951 CCTGGTGGAA TTTGAAAAAC TCATAGAGAA ACTGAGAGAA TCCCCTTCGT
1001 TCGCCATAGA TCTTGAGACG TCTTCCCTCG ATCCTTTCGA CTGCGACATT
1051 GTCGGTATCT CTGTGTCTTT CAAACCAAAG GAAGCGTACT ACATACCACT
1101 CCATCATAGA AACGCCCAGA ACCTGGATGA AAAAGAAGTT CTGAAAAAGC
1151 TAAAAGAAAT CCTGGAGGAC CCCGGAGCAA AGATCGTTGG TCAGAATTG
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1251 TCACTTCGAC ACGATGATAG CGGCTTACCT TCTTGAGCCG AACGAAAAGA
1301 AGTTCAATCT GGACGATCTC GCATTGAAAT TTCTTGATA CAAAATGACC
1351 TCTTACCAGG AACTCATGTC CTTCTCTTCT CCGCTGTTTG GTTTCAGTTT
1401 TGCCGATGTT CCTGTAGAAA AAGCAGCGAA CTATTCCTGT GAAGATGCAG
1451 ACATCACCTA CAGACTCTAC AAGATCCTGA GCTTAAACT CCACGAGGCA
1501 GATCTGGAGA ACGTGTCTA CAAGATAGAA ATGCCTCTTG TGAGCGTGCT
1551 TGCACGGATG GAACTGAACG GTGTGCGCCT GGACGTGGCC TATCTCAGGG
1601 CCTTGTCCTT GGAGGTGGCC GAGGAGATCG CCCGCCTCGA GGCCGAGGTC
1651 TTCCGCCTGG CCGGCCACCC CTTCAACCTC AACTCCCGGG ACCAGCTGGA
1701 AAGGGTCCTC TTTGACGAGC TAGGGCTTCC CGCCATCGGC AAGACGGAGA
1751 AGACCGGCAA GCGCTCTACC AGCGCCGCCG TCCTGGAGGC CCTCCGCGAG
1801 GCCACCCCA TCCTGGAGAA GATCCTGCAG TACCGGGAGC TCACCAAGCT
1851 GAAGAGCACC TACATTGACC CTTGCCGGA CCTCATCCAC CCCAGGACGG
1901 GCCGCCTCCA CACCCGCTTC AACCAGACGG CCACGGCCAC GGGCAGGCTA
1951 AGTAGCTCCG ATCCCAACCT CCAGAACATC CCCGTCCGCA CCCCCTTGG
2001 GCAGAGGATC CGCCGGGCTT TCATCGCCGA GGAGGGGTGG CTATTGGTGG
2051 CCCTGGACTA TAGCCAGATA GAGCTCAGGG TGCTGGCCCA CCTCTCCGGC
2101 GACGAGAACC TGATCCGGGT CTTCCAGGAG GGGCGGGACA TCCACACGGA
2151 GACCGCCAGC TGGATGTTCT GCGTCCCCCG GGAGGCCGTG GACCCCTGA
2201 TGCGCCGGGC GGCCAAGACC ATCAACTTCG GGGTCCTCTA CGGCATGTCTG
2251 GCCACCGCC TCTCCAGGA GCTAGCCATC CTTACGAGG AGGCCAGGC
2301 CTTCATTGAG CGCTACTTTC AGAGCTTCCC CAAGGTGCGG GCCTGGATTG
2351 AGAAGACCTT GGAGGAGGGC AGGAGGCGGG GGTACGTGGA GACCTCTTTC
2401 GGCCGCCGCC GCTACGTGCC AGACCTAGAG GCCCGGGTGA AGAGCGTGCG
2451 GGAGGCGGCC GAGCGCATGG CTTCAACAT GCCCGTCCAG GGCACGCCCG
2501 CCGACCTCAT GAAGCTGGCT ATGGTGAAGC TCTTCCCAG GCTGGAGGAA

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Figure 4/2  
SEQ ID No.: 4

2551 ATGGGGGCCA GGATGCTCCT TCAGGTCCAC GACGAGCTGG TCCTCGAGGC  
2601 CCCAAAAGAG AGGGCGGAGG CCGTGGCCCCG GCTGGCCAAG GAGGTCATGG  
2651 AGGGGGTGTA TCCCCTGGCC GTGCCCTGG AGGTGGAGGT GGGGATAGGG  
2701 GAGGACTGGC TCTCCGCCAA GGAGTGA

SEQ ID NO.: 10

amino acid sequence:

1 MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL  
51 TTSRGEVPQA VYGFAKSLLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA  
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG  
151 YEVRILTADK DLYQLLSMRI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR  
201 ALTGDESDNL PGVKGIGECT ARKLLEEWGS LEALLKNLDR LKPAIRKIL  
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH  
301 EFGLLESPPV **GYRIVKDLVE FEKLIEKLRE SPSFAIDLET SSLDPFDCHI**  
351 VGISVSFKPK EAYYIPLHHR NAQNLDEKEV LKKLKEILED PGAKIVGQNL  
401 KFDYKVLNVK GVEPVPPHFD TMIAAYLLEP NEKKFNLDL ALKFLGYKMT  
451 SYQELMSFSS PLFGFSFADV PVEKAANYSC EDADITYRLY KILSLKLHEA  
501 **DLENVYKIE MPLVSVLARM ELNGVRLDVA YLRALSLEVA EEIARLEAEV**  
551 FRLAGHPFNL NSRDQLERVL FDELGLPAIG KTEKTGKRST SAAVLEALRE  
601 AHPIVEKILQ YRELTCLKST YIDPLPLIH PRTGRLHTRF NQTATATGRL  
651 SSSDPNLQNI PVRTPLGQRI RRAFIAEEGW LLVALDYSQI ELRVLAHLG  
701 DENLIRVFQE GRDIHTETAS WMFGVPREAV DPLMRRAAKT INFGVLYGMS  
751 AHRLSQELAI PYEEAQAFIE RYFQSFPKVR AWIEKTLEEG RRRGYVETLF  
801 GRRRYVPDLE ARVKSUREAA ERMAFNMPVQ GTAADLMKLA MVKLFPRLEE  
851 MGARMLLQVH DELVLEAPKE RAEAVARLAK EVMEGVYPLA VPLEVEVGIG  
901 EDWLSAKE



Figure 5/1  
SEQ ID No.: 5

DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCTCTCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCTGGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCTCTC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCC ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAG CCCCCATCCA GCAGTTGTGG ACATCTTCGA
951 ATACGATATT CCATTTGCAA AGAGATACCT CATCGACAAA GGCCTAATAC
1001 CAATGGAGGG GGAAGAAGAG CTAAAGATTG TTGCCTTCGA TATAGAAACC
1051 CTCTATCACG AAGGAGAAGA GTTTGGAAAA GGCCCAATTA TAATGATTAG
1101 TTATGCAGAT GAAAATGAAG CAAAGGTGAT TACTTGAAA AACATAGATC
1151 TTCCATACGT TGAGGTTGTA TCAAGCGAGA GAGAGATGAT AAAGAGATTT
1201 CTCAGGATTA TCAGGGAGAA GGATCCTGAC ATTATAGTTA CTTATAATGG
1251 AGACTCATTC GACTTCCCAT ATTTAGCGAA AAGGGCAGAA AAACCTGGGA
1301 TTAAATTAAC CATTGGAAGA GATGGAAGCG AGCCCAAGAT GCAGAGAATA
1351 GGCGATATGA CGGCTGTAGA AGTCAAGGGA AGAATACATT TCGACTTGTA
1401 TCATGTAATA ACAAGGACAA TAAATCTCCC AACATACACA CTAGAGGCTG
1451 TATATGAAGC AATTTTTTGA AAGCCAAAGG AGAAGGTATA CGCCGACGAG
1501 ATAGCAAAAG CCTGGGAAAG TGGAGAGAAC CTTGAGAGAG TTGCCAAATA
1551 CTCGATGGAA GATGCAAAGG CAACTTATGA ACTCGGGAAA GAATTCCTTC
1601 CAATGGAAAT TCAGCTTTCA GAGAGGCTCC TTTGGCTTTA CCGGGAGGTG
1651 GAGAGGCCCC TTTCCGCTGT CCTGGCCCAC ATGGAGGCCA CGGGGGTGCG
1701 CCTGGACGTG GCCTATCTCA GGGCCTTGTC CCTGGAGGTG GCCGAGGAGA
1751 TCGCCCGCCT CGAGGCCGAG GTCTTCCGCC TGGCCGGCCA CCCCTTCAAC
1801 CTCAACTCCC GGGACCAGCT GGAAAGGGTC CTCTTTGACG AGCTAGGGCT
1851 TCCCGCCATC GGCAAGACGG AGAAGACCGG CAAGCGCTCC ACCAGCGCCG
1901 CCGTCTGGA GGCCCTCCGC GAGGCCACCC CCATCGTGGA GAAGATCCTG
1951 CAGTACCGGG AGCTACACAA GCTGAAGAGC ACCTACATTG ACCCCTTGCC
2001 GGACCTCATC CACCCCAGGA CGGGCCGCCT CCACACCCGC TTCAACCAGA
2051 CGGCCACGGC CACGGGCAGG CTAAGTAGCT CCGATCCCAA CCTCCAGAAC
2101 ATCCCCGTCC GCACCCCGCT TGGGCAGAGG ATCCGCCGGG CCTTCATCGC
2151 CGAGGAGGGG TGCTATTGG TGGCCCTGGA CTATAGCCAG ATAGAGCTCA
2201 GGGTGCTGGC CCACCTCTCC GGCGACGAGA ACCTGATCCG GGTCTTCCAG
2251 GAGGGGCGGG ACATCCACAC GGAGACCGCC AGCTGGATGT TCGGCGTCCC
2301 CCGGGAGGCC GTGGACCCCC TGATGCGCCG GGCGGCCAAG ACCATCAACT
2351 TCGGGGTCCT CTACGGCATG TCGGCCACC GCCTCTCCA GGAGCTAGCC
2401 ATCCCTTACG AGGAGGCCCA GGCTTCATT GAGCGCTACT TTCAGAGCTT
2451 CCCCAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC
2501 GGGGGTACGT GGAGACCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA

```

Figure 5/2  
SEQ ID No.: 5

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2551 GAGGCCCGGG TGAAGAGCGT GCGGGAGGCG GCCGAGCGCA TGGCCTTCAA
2601 CATGCCCGTC CAGGGCACCG CCGCCGACCT CATGAAGCTG GCTATGGTGA
2651 AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT CCTTCAGGTC
2701 CACGACGAGC TGGTCCTCGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC
2751 CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCCTG GCCGTGCCCC
2801 TGGAGGTGGA GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA

```

SEQ ID No.: 11

amino acid sequence:

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1  MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51  TTSRGEVPQA VYGFAKSLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTPEDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLLSMRI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGKEK ARKLLEEWGS LEALLKNLDR LKPAIREKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLLH
301 EFGLESPPH AVVDIFEYDI PFAKRYLIDK GLIPMEGEEE LKILAFDIET
351 LYHEGEEFGK GPIIMISYAD ENEAKVITWK NIDLPHYVEV SSEREMIKRF
401 LRIIREKDPD IIVTYNGDSF DFPYLAKRAE KLGIKLTIGR DGSEPKMQRI
451 GDMTAVEVKG RIHFDLYHVI TRTINLPTYT LEAVYEAIFG KPKEKVYADE
501 IAKAWESGEN LERVAKYSME DAKATYELGK EFLPMEIQLS ERLLWLRYEV
551 ERPLSAVLAH MEATGVRLDV AYLRALSLEV AEEIARLEAE VFRLAGHPFN
601 LNSRDQLERV LFDELGLPAI GKTEKTGKRS TSAAVLEALR EAHPIVEKIL
651 QYRELTKLKS TYIDPLPDLI HPRTGRLHTR FNQTATATGR LSSSDPNLQN
701 IPVRTPLGQR IRRAFIAEEG WLLVALDYSQ IELRVLAHLS GDENLIRVFQ
751 EGRDIHTETA SWMFGVPREA VDPLMRRAAK TINFGVLYGM SAHRLSQELA
801 IPYEEAQAFI ERYFQSFPKV RAWIEKTEE GRRRGYVETL FGRRRYVPDL
851 EARVKSUREA AERMAFNMPV QGTAADLMKL AMVKLFPRLE EMGARMLLQV
901 HDELVLAPK ERAEAVARLA KEVMEGVYPL AVPLEVEVGI GEDWLSAKE*

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Figure 6/1  
SEQ ID No.: 6

DNA sequence:

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1  ATGAGGGGCT CGCATCACCA TCACCATCAC GCTGCTGACG ATGACGATAA
51  AATGAGGGGC ATGCTACCGC TATTTGAGCC CAAGGGCCGG GTCCTCCTGG
101 TCGACGGCCA CCACCTGGCC TACCGCACCT TCCACGCCCT GAAGGGCCTC
151 ACCACCAGCC GGGGGGAGCC GGTGCAGGCG GTCTACGGCT TCGCCAAGAG
201 CCTCCTCAAG GCCCTCAAGG AGGACGGGGA CGCGGTGATC GTGGTCTTTG
251 ACGCCAAGGC CCCCTCCTTC CGCCACGAGG CCTACGGGGG GTACAAGGCG
301 GGCCGGGCCC CCACGCCGGA GGACTTTCCC CGGCAACTCG CCCTCATCAA
351 GGAGCTGGTG GACCTCCTGG GGCTGGCGCG CCTCGAGGTC CCGGGCTACG
401 AGGCGGACGA CGTCCTGGCC AGCCTGGCCA AGAAGGCGGA AAAGGAGGGC
451 TACGAGGTCC GCATCCTCAC CGCCGACAAA GACCTTTACC AGCTCCTTTC
501 CGACCGCATC CACGTCTTCC ACCCCGAGGG GTACCTCATC ACCCCGGCCT
551 GGCTTTGGGA AAAGTACGGC CTGAGGCCCG ACCAGTGGGC CGACTACCGG
601 GCCCTGACCG GGGACGAGTC CGACAACCTT CCCGGGGTCA AGGGCATCGG
651 GGAGAAGACG GCGAGGAAGC TTCTGGAGGA GTGGGGGAGC CTGGAAGCCC
701 TCCTCAAGAA CCTGGACCGG CTGAAGCCCG CCATCCGGGA GAAGATCCTG
751 GCCCACATGG ACGATCTGAA GCTCTCCTGG GACCTGGCCA AGGTGCGCAC
801 CGACCTGCCC CTGGAGGTGG ACTTCGCCAA AAGGCGGGAG CCCGACCGGG
851 AGAGGCTTAG GGCCTTTCTG GAGAGGCTTG AGTTTGGCAG CCTCCTCCAC
901 GAGTTCGGCC TTCTGGAAAG CCCC GTTAGA GAACATCCAG CAGTTGTGGA
951 CATCTTCGAA TACGATATTC CATTTGCAAA GAGATACCTC ATCGACAAAG
1001 GCCTAATACC AATGGAGGGG GAAGAAGAGC TAAAGATTCT TGCCTTCGAT
1051 ATAGAAACCC TCTATCACGA AGGAGAAGAG TTTGGAAAAG GCCCAATTAT
1101 AATGATTAGT TATGCAGATG AAAATGAAGC AAAGGTGATT ACTTGGA AAA
1151 ACATAGATCT TCCATACGTT GAGGTGTAT CAAGCGAGAG AGAGATGATA
1201 AAGAGATTTT TCAGGATTAT CAGGGAGAAG GATCCTGACA TTATAGTTAC
1251 TTATAATGGA GACTCATTCG ACTTCCCATA TTTAGCGAAA AGGGCAGAAA
1301 AACTTGGGAT TAAATTAACC ATTGGAAGAG ATGGAAGCGA GCCCAAGATG
1351 CAGAGAATAG GCGATATGAC GGCTGTAGAA GTCAAGGGAA GAATACATTT
1401 CGACTTGTAT CATGTAATAA CAAGGACAAT AAATCTCCCA ACATACACAC
1451 TAGAGGCTGT ATATGAAGCA ATTTTGGAA AGCCAAAGGA GAAGGTATAC
1501 GCCGACGAGA TAGCAAAAGC CTGGGAAAGT GGAGAGAACC TTGAGAGAGT
1551 TGCCAAATAC TCGATGGAAG ATGCAAAAGC AACTTATGAA CTCGGGAAAG
1601 AATTCCTTCC AATGGAAATT CAGCTTTCAA GATTAGTTGG ACAACCTTTA
1651 TGGGATGTTT CAAGGTCAAG CACAGGGAAC CTTGTAGAGT GGTTCTTACT
1701 TAGGAAAGCC TACGAAAGAA ACGAAGTAGC TCCAAACAAG CCAAGTGAAG
1751 AGGAGTATCA AAGAAGGCTC AGGGAGAGCT ACACAGGTGG ATTCGTGCGC
1801 CTGGACGTGG CCTATCTCAG GGCCTTGTC CTGGAGGTGG CCGAGGAGAT
1851 CGCCCGCCTC GAGGCCGAGG TCTTCCGCTT GGCCGGCCAC CCCTTCAACC
1901 TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA GCTAGGGCTT
1951 CCCGCCATCG GCAAGACGGA AAGACCGGC AAGCGCTCCA CCAGCGCCGC
2001 CGTCCTGGAG GCCCTCCGCG AGGCCACCC CATCGTGGAG AAGATCCTGC
2051 AGTACCGGGA GCTACCAAG CTGAAGAGCA CCTACATTGA CCCCTTGCCG
2101 GACCTCATCC ACCCCAGGAC GGGCCGCCTC CACACCCGCT TCAACCAGAC
2151 GGCCACGGCC ACGGGCAGGC TAAGTAGCTC CGATCCCAAC CTCCAGAACA
2201 TCCCCGTCCG CACCCGCTT GGGCAGAGGA TCCGCCGGGC CTTTCATCGCC
2251 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG
2301 GGTGCTGGCC CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG
2351 AGGGGCGGGA CATCCACACG GAGACCGCCA GCTGGATGTT CGGCGTCCCC
2401 CGGGAGGCCG TGGACCCCTT GATGCGCCGG GCGGCAAGA CCATCAACTT
2451 CGGGGTCTTC TACGGCATGT CGGCCACCG CCTCTCCAG GAGCTAGCCA
2501 TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT TCAGAGCTTC

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Figure 6/2  
SEQ ID No.: 6

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2551 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG
2601 GGGGTACGTG GAGACCCTCT TCGGCCGCCG CCGCTACGTG CCAGACCTAG
2651 AGGCCCGGGT GAAGAGCGTG CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC
2701 ATGCCCGTCC AGGGCACCGC CGCCGACCTC ATGAAGCTGG CTATGGTGAA
2751 GCTCTTCCCC AGGCTGGAGG AAATGGGGGC CAGGATGCTC CTTCAGGTCC
2801 ACGACGAGCT GGTCTCGAG GCCCAAAG AGAGGGCGGA GGCCGTGGCC
2851 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCCT
2901 GGAGGTGGAG GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGA

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SEQ ID No.: 12

amino acid sequence:

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1 MRGSHHHHHH AADDDDKMRG MLPLFEPKGR VLLVDGHHLA YRTFHALKGL
51 TTSRGEVQA VYGFAKSLK ALKEDGDAVI VVFDKAPSF RHEAYGGYKA
101 GRAPTEPDFP RQLALIKELV DLLGLARLEV PGYEADDVLA SLAKKAEKEG
151 YEVRILTADK DLYQLSDRI HVLHPEGYLI TPAWLWEKYG LRPDQWADYR
201 ALTGDESDNL PGVKGIGECT ARKLEEWGS LEALLKNLDR LKPAIRKIL
251 AHMDDLKLSW DLAKVRTDLP LEVDFAKRRE PDRERLRAFL ERLEFGSLH
301 EFGLLESPVR EHPAVVDIFE YDIPFAKRYL IDKGLIPMEG EEELKILAFD
351 IETLYHEGEE FGKGPIIMIS YADENEAKVI TWKNIDLPIV EVVSSEREMI
401 KRFLRIIREK DPDIIVTYNG DSFDFFPYLAK RAEKLGKILT IGRDGSEPKM
451 QRIGDMTAVE VKGRIHFDLY HVITRTINLP TYTLEAVYEA IFGKPKEKVY
501 ADEIAKAWES GENLERVAKY SMEDAKATYE LGKEFLPMEI QLSRLVGQPL
551 WDVSRSSSTGN LVEWFLLRKA YERNEVAPNK PSEEEYQRRL RESYTGGFVR
601 LDVAYLRALS LEVAEEIARL EAEVFERLAGH PFNLNSRDQL ERVLFDELGL
651 PAIGKTEKTG KRSTSAAVLE ALREAHPIVE KILQYRELTK LKSTYIDPLP
701 DLIHPRTGRL HTRFNQTATA TGRLLSSSDPN LQNIPTVRTPL GQIRIRAFIA
751 EEGWLLVALD YSQIELRVLA HLSGDNELIR VFQEGRDIHT ETASWMFGVP
801 REAVDPLMRR AAKTINFGVL YGMSAHRLSQ ELAIPYEEAQ AFIERYFQSF
851 PKVRAWIEKT LEEGRRRGYV ETLFGRRRYV PDLEARVKS SV REAAERMAFN
901 MPVQGTADL MKLAMVKLFP RLEEMGARM LQVHDELVL EAPKERA EAVA
951 RLAKEVMEGV YPLAVPLEVE VGIGEDWLSA KE*

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Figure 7

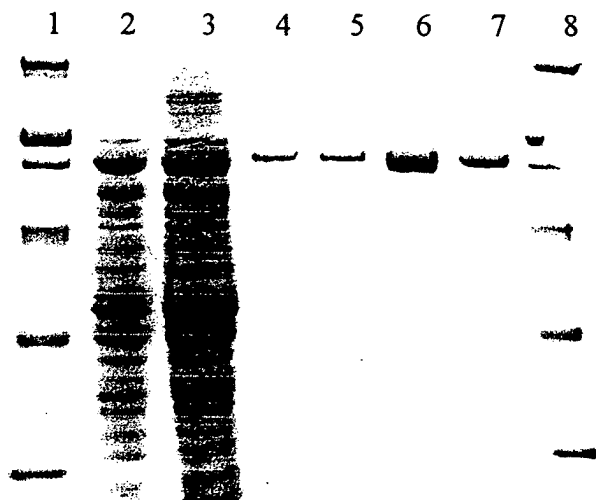


Figure 8

09/623326

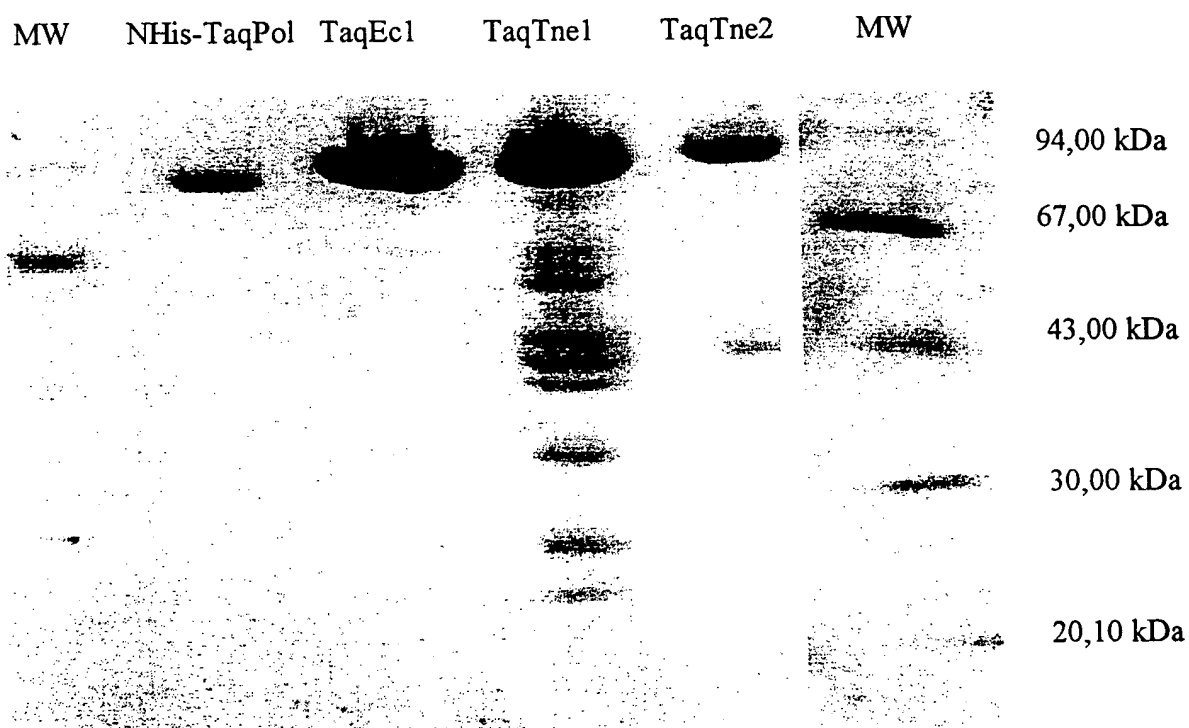


Figure 9

09/623326

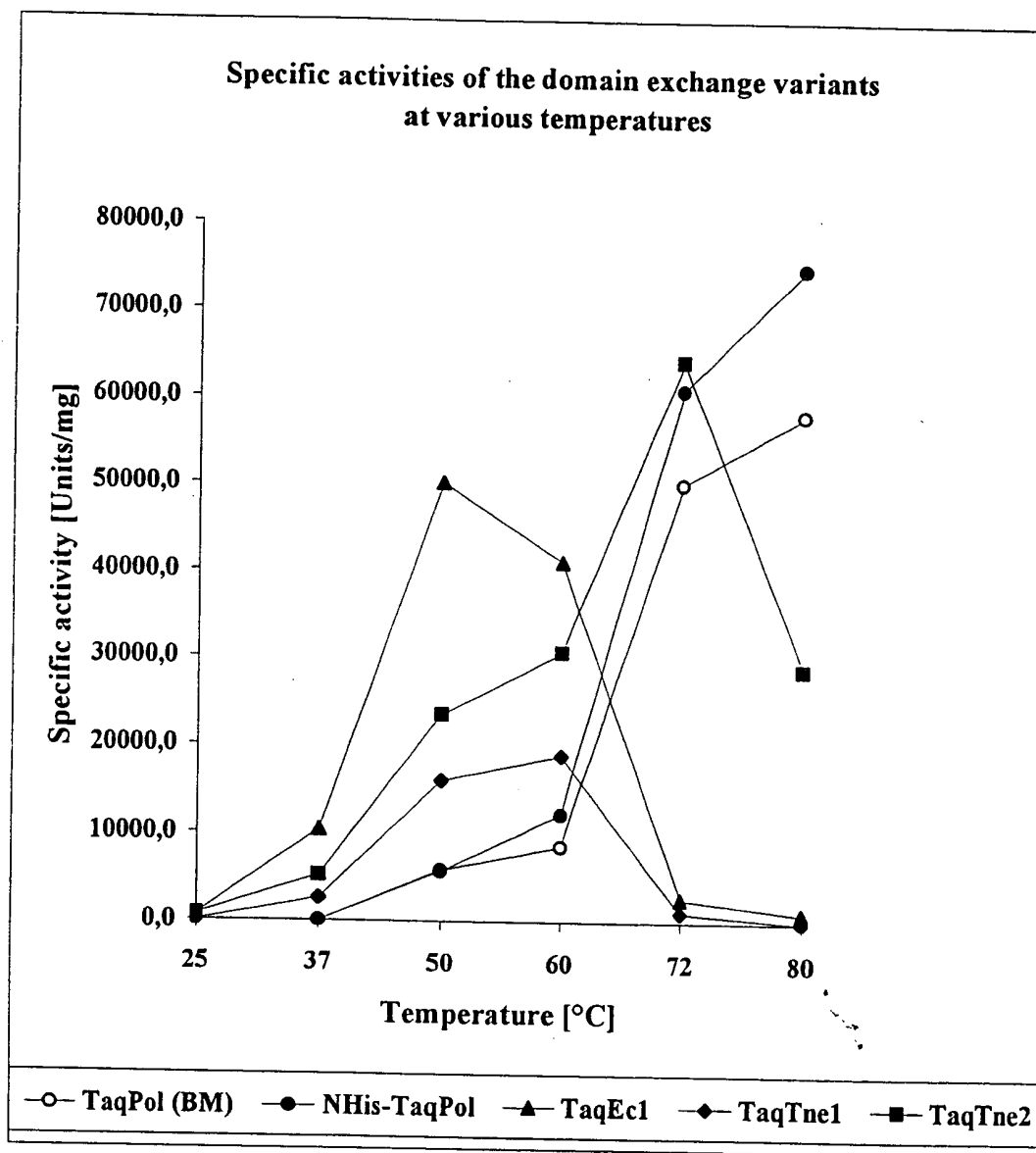


Figure 10

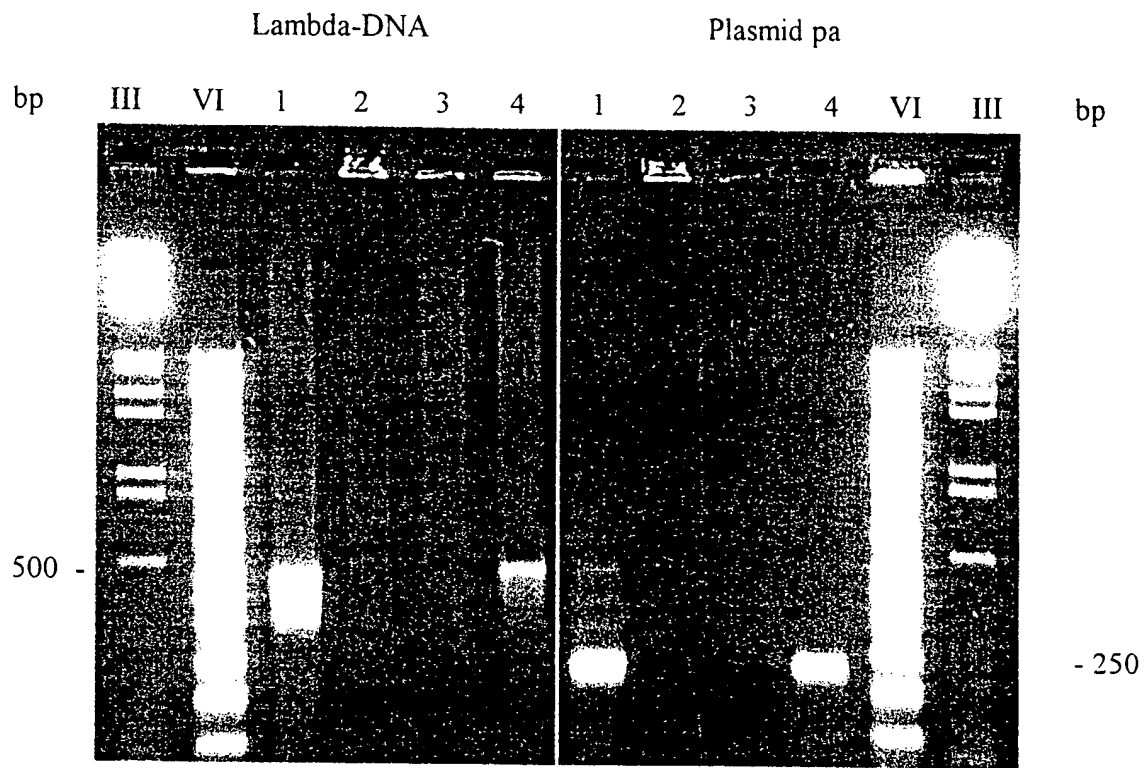




Figure 11

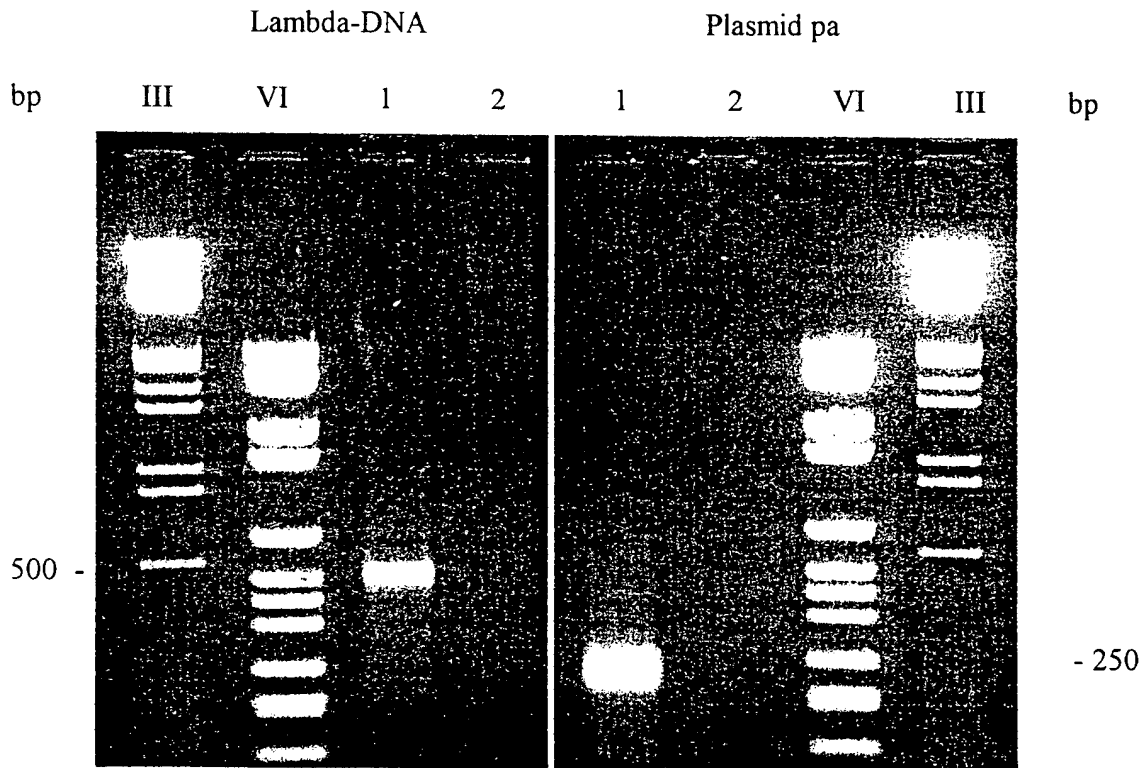


Figure 12

09/623326

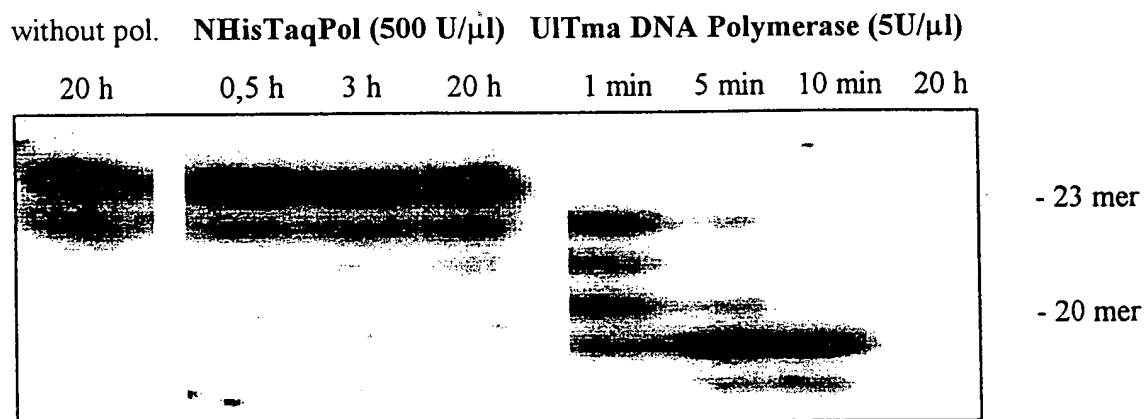
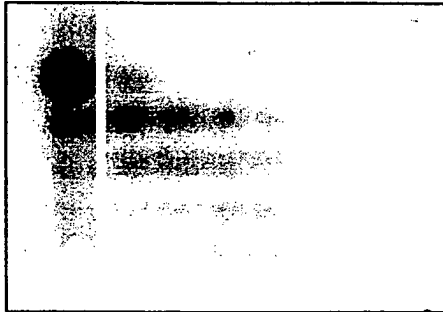


Figure 13

09/623326

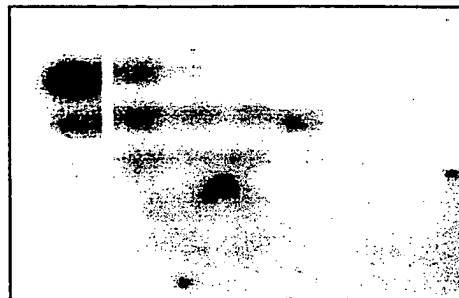
without pol. TaqEc1 (500 U/ $\mu$ l)

600 15 30 45 60 90 180 600 min



ohne Pol TaqEc1 (500 U/ $\mu$ l)

600 15 30 45 60 90 180 600 min



- 23 mer

- 20 mer

Figure 14

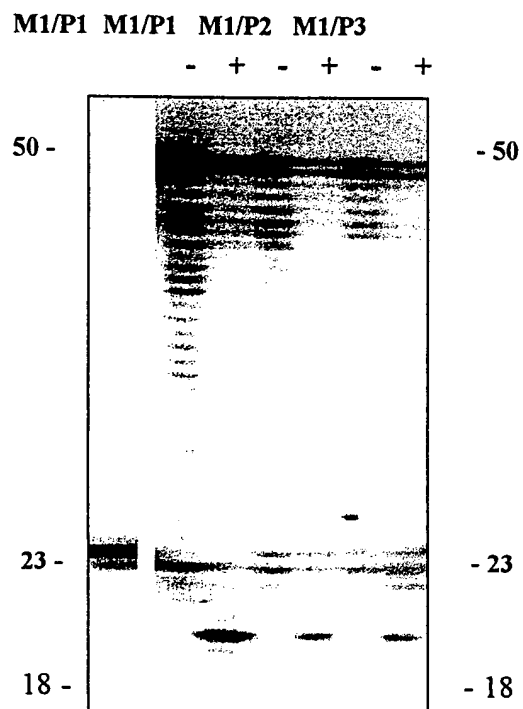


Figure 15

Degradation of primers at the 3'-end (3'-5' exonuclease assay)  
and  
Correction of 3'-mismatched Primers and their extension (3'-mismatch primer correction assay)

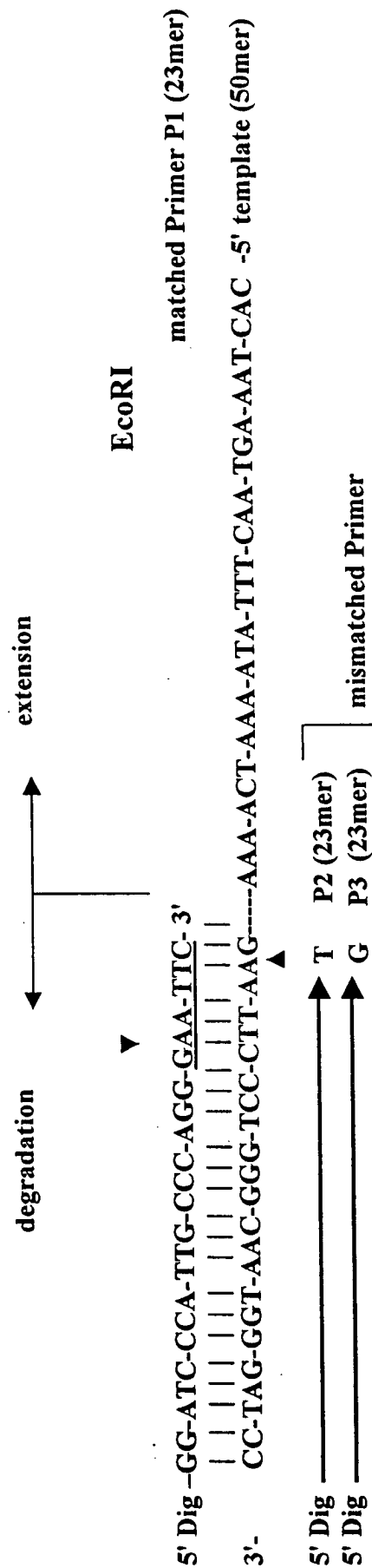


Figure 16

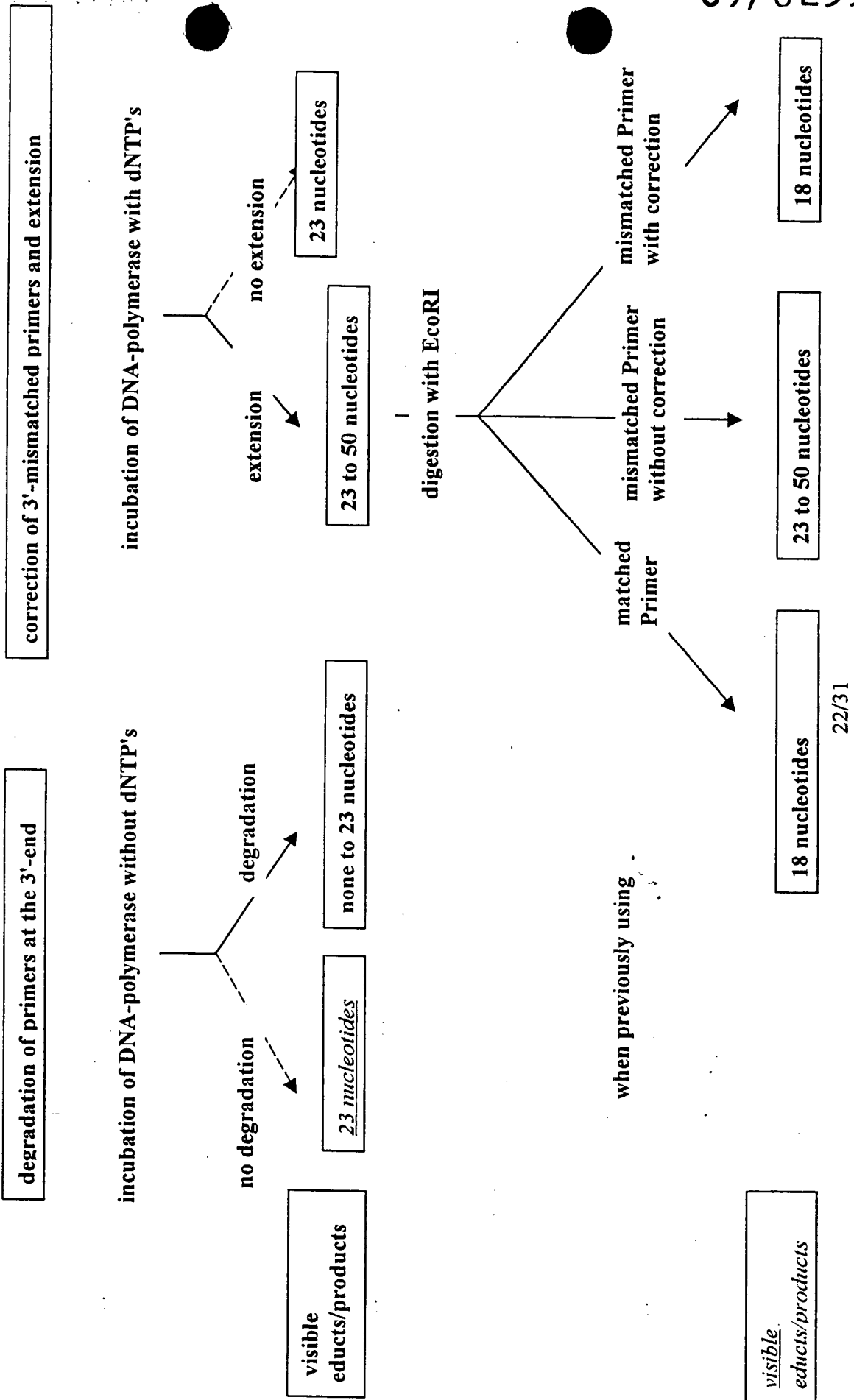


Fig. 17/1

SEQ ID No. 43  
 SEQ ID No. 44  
 SEQ ID No. 45  
 SEQ ID No. 46

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chimera_____ ----MARLFLFDGTALAYRAYYALDRSLSTSTGIPTNATYGVARMLVRFIKDHIIVGKD
tne.rse_____ ----MARLFLFDGTALAYRAYYALDRSLSTSTGIPTNATYGVARMLVRFIKDHIIVGKD
ath.rse_____ ----MKLVIFDGNLSILYRAFFALP-ELTTSNNIPTNAIYGfVNVILKYLEQ---EKPD
DPO1_ECOLI MVQIPQNPLILVDGSSYLRYAHAF-PLTNSAGEPTGAMYGVNLMLRSLIMQ---YKPT
               * . ** . ***. *   *..* . ***. * * . .

chimera_____ YVAVAFDKKAATFRHKLLETYKAQRPKTPDLLIQQLPYIKKLVEALGMKVLEVEGYEADD
tne.rse_____ YVAVAFDKKAATFRHKLLETYKAQRPKTPDLLIQQLPYIKKLVEALGMKVLEVEGYEADD
ath.rse_____ YVAVAFDKRGREARKSEYEYKANRKPMPDNLQVQIPYVREILYAFNIPIIEFEGYEADD
DPO1_ECOLI HAADVFDAGKKTFRDELFEHYKSHRPPMPDDLRAQIEPLHAMVKAMGLPLLAVSGVEADD
               ** ** .   *   * ** . *   ** * * . . . . * . . . . * ****

chimera_____ IIATLAVKGLPLFDEIFIVTGDKDMLQLVNEKIKVWRIVKGISD--LELYDAQKVKEKYG
chimera_____ IIATLAVKGLPLFDEIFIVTGDKDMLQLVNEKIKVWRIVKGISD--LELYDAQKVKEKYG
ath.rse_____ VIGSLVNQFKNTGLDIVIITGDRDTLQLLDKNVVKIVSTKFDKTVEDLYTVENVKEKYG
DPO1_ECOLI VIGTLAREAEKAGRPVLISTGDKDMAQLVTPNITLINTMTNTILG--PE----EVVNKYG
               . * . * .   * ****. * ** . . . . * ****

chimera_____ VEPQQIPDLLALTGDEIDNIPGVTGIGEKTA VQ LLEKYKDLEDILNHVREL P-----Q
tne.rse_____ VEPQQIPDLLALTGDEIDNIPGVTGIGEKTA VQ LLEKYKDLEDILNHVREL P-----Q
ath.rse_____ VWANQVPDYKALVGDQSDNIPGVKGIGEKSAQKLLEEYSSLEEIYQNLDKIK-----S
DPO1_ECOLI VPPELIIDFLALMGDSSDNIPGVPGVEKTAQALLQGLGLDTLYAEPEKIAGLSFRGAK
               * .   * ** ** ***** * . ***. * ** .   * . . .

chimera_____ KVRKALLRDRENAILS SKKLAIETNVPIEINWHEELRYQGYDREKLLPLLKELEFASIMKE
tne.rse_____ KVRKALLRDRENAILS SKKLAIETNVPIEINWHEELRYQGYDREKLLPLLKELEFASIMKE
ath.rse_____ SIREKLEAGKDMAFLSKRLATIVCDLPLNVKLEDLRTKEWNKERLYEILVQLEFKSIIKR
DPO1_ECOLI TMAAKLEQNKEVAYLSYQLATIKTDVELELTCEQLEVQQPAEELLGLFKKYEFKRWTAD
               .   *   .. * ** . ** . . . . . * * .   * * .   **

chimera_____ LQLYEESEPVGYRIVK-----DIVEFEKLIKLEKRESP
tne.rse_____ LQLYEESEPVGYRIVK-----DIVEFEKLIKLEKRESP
ath.rse_____ LGLS-----EVVQFEFVQQRDIPD
DPO1-ECOLI VEAGKWLQAKGAKPAAKPQETSVADEAPEVTATVISYDNYVTILDEETLKAWIAKLEKAP
               .

chimera_____ SFAIDLETSSLDPFDCDIVGISVSFKPKAEAYYIPLHHRNAQNLDKE---VLKKLKEILE
tne.rse_____ SFAIDLETSSLDPFDCDIVGISVSFKPKAEAYYIPLHHRNAQNLDKE---VLKKLKEILE
ath.rse_____ VEQKELESISQIRSKE--IPLMFVQGEK-CFYLYDQESNTVFITSN-----KLLIEEIL
DPO1_ECOLI VFAFDTETDSDLNISANLVGLSFAIEPGVAAYIPVAHDYLDAPDQISRERALELLKPLLE
               . * . * . . . . . * .   * .

```

Fig. 17/2

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1\_ECOLI

DPGAKIVGQNLKFDYKVLMMVGVEPVPPHFDTMIAAYLLEPNEKKFNLDLALKFLGYKM  
DPGAKIVGQNLKFDYKVLMMVGVEPVPPHFDTMIAAYLLEPNEKKFNLDLALKFLGYKM  
KSDTVKIMYDLKNI FHQLNLEDTNNIKNCEDVMIASYVLDSTRSSYELETFLVSYLNTDI  
DEKALKVGQNLKYDRGILANYGIELRGIAFDTMLESYILNSVAGRHDMSLAERWLKHKT  
\* \* \* \* \*

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1\_ECOLI

TSYQELMSFSSPLFGFSFADVPVEKAANYSCEDADITYRLYKILSLKLHEAD-LENVFYK  
TSYQELMSFSSPLFGFSFADVPVEKAANYSCEDADITYRLYKILSLKLHEAD-LENVFYK  
EAVKKDKKIVS-----VLLKRLWDELLRLIDLNS-CQFLYEN  
ITFEEIAGKGKNQ--LTFNQIALEEAGRYAAEDADVTQLHLKMWPDQLQKHGKPLNVFEN  
\* \* \* \* \*

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1-ECOLI

IEMPLVSVLARMELNGVKVDRDALIQYTKEIENKILKLETQIYQIAGEWFNINSPKQLSY  
IEMPLVSVLARMELNGVYVDTEFLKKLSEEYGGKLEELAEIYRIAGEPNINSPKQVSR  
IERPLIPVLYEMEKTFGKVDRDALIQYTKEIENKILKLETQIYQIAGEWFNINSPKQLSY  
IEMPLVPVLSRIERNVGKIDPKVLHNNHSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQT  
\* \* \* \* \*

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1\_ECOLI

ILFEKLKLPVIKKTGTG--YSTDAEVLEELFDKHEIVPLILDYRMYTKILTYYCQGLLQA  
ILFEKLGIKPRGKTTKTGDYSTRIEVLEELAGEHEIIPILILEYRKIQKLKSTYIDALPKM  
ILFEKLKLPVIKKTGTG--YSTDAEVLEELFDKHEIVPLILDYRMYTKILTYYCQGLLQA  
ILFEKQGIKPLKKTGG-APSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKPLPM  
\* \* \* \* \*

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1-ECOLI

INPSSGRVHTTFIQTGTATGRLESSDPNLQNI PVKYDEGKLIRKVFVPEG-GHVLIDADY  
VNPKTGRIHASFNQTGTATGRLESSDPNLQNLPTKSEEGKEIRKAIVPQDPNWWIVSADY  
INPSSGRVHTTFIQTGTATGRLESSDPNLQNI PVKYDEGKLIRKVFVPEG-GHVLIDADY  
INPKTGRVHTSYHQA VTATGRLSSTDPNLQNI PVRNEEGRRIRQAFIAPE-DYVIVSADY  
\* \* \* \* \*

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1\_ECOLI

SQIELRILAHISEDRLISAFKNNVDIHSQTAAEVFGVDIADVTPEMRSQAKAVNFGIVY  
SQIELRILAHLSGDNLLRAFEEGIDVHTLTASRIFNVKPEEVTEEMRRAGKMNFSIY  
SQIELRILAHISEDRLISAFKNNVDIHSQTAAEVFGVDIADVTPEMRSQAKAVNFGIVY  
SQIELRIMAHLSRDKGLLTAFAGKDIHRATAAEVFGVPLET VTSEQRSAKAINFGLIY  
\* \* \* \* \*

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1\_ECOLI

GISDYGLARDIKISRKEAAEFINKY FERYPKVKEYLDNTV KFARDNGFVLTFLNRKRYIK  
GVTPYGLSVRLGVPVKEAEKMIVNYFVLYPKVRDYIQRVVSEAKEKGYVRTLFGRKRDIP  
GISDYGLARDIKISRKEAAEFINKY FERYPKVKEYLDNTV KFARDNGFVLTFLNRKRYIK  
GMSAFGLARQLNIPRKEAQKYMDLY FERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLP  
\* \* \* \* \*

chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1\_ECOLI

DIKSTNRNLRGYAERIA MNSPIQGSAADIMKLAMIKVYQKLKENNLKSKII LQVHDELLI  
QLMARDNTQAEGERIAINTPIQGTAA DI IKLAMIEIDRELKERKMRSKMII QVHDELVF  
DIKSTNRNLRGYAERIA MNSPIQGSAADIMKLAMIKVYQKLKENNLKSKII LQVHDELLI  
DIKSSNGARRAAAERA AINAPMQGTAA DI IKRAMIAVDWLQAEQPRVRMIMQVHDELVF  
\* \* \* \* \*



chimera\_\_\_\_  
tne.rse\_\_\_\_  
ath.rse\_\_\_\_  
DPO1\_ECOLI

EAPYEEKDIVKEIVKREMANAVALKVPLVVEVKEGLNWEYENKI  
EVPNEEKDALVELVKDRMTNVVKLSVPLEVDVTIGKTWS----  
EAPYEEKDIVKEIVKREMANAVALKVPLVVEVKEGLNWEYENKI  
EVHKDDVDAAKQIHQLMENCTRLDVPLLVEVGSGENWDQAH-  
\* .. \* . . . \* \* \* \* \* \* \* \*

Figure 18/1:

SEQ ID No.: 19

SEQ ID No.: 20

SEQ ID No.: 21

SEQ ID NO.: 22

TNE UP 5' CTG ACC ATG GCG AGA CTA TTT CTC TTT G -3'  
 TNE LOW 5' TCT GTC GAC CTT CAC ACC GTT CAG TTC CAT CC -3'  
 ATH UP 5' - AAG GTC GAC AGA GAT GCC CTC ATC CAA TAT ACC -3'  
 ATH LOW 5' - TAG CAA GCT TCT ATT TTG TCT CAT ACC AGT -3'

A.

crossing point 1

SEQ ID No.: 23

SEQ ID No.: 24

SEQ ID No.: 25

chimera\_\_8 IEMPLVSVLARMELNGV | KVDRDALIQYTKIEINKILKLETQIYQIAGEWFNINSPKQLSY  
 tne.rse\_\_ IEMPLVSVLARMELNGV | YVDTEFLKKLSEYGGKLEELAEIYRIAGEPFNINSPKQVSR  
 ath.rse\_\_ IERPLIPVLYEMEKTGF | KVDRDALIQYTKIEINKILKLETQIYQIAGEWFNINSPKQLSY

B.

SEQ ID No.: 19

SEQ ID No.: 26

SEQ ID No.: 27

5' ctg acc ATG GCG AGA CTA TTT CTC TTT G -3'  
 TNEUP |----->  
 ATG GCG AGA CTA TTT CTC TTT GAT GGA 27  
 M A R L F L F D G 9

1

SEQ ID No.: 28

SEQ ID No.: 29

SEQ ID No.: 20

SEQ ID No.: 21

SEQ ID No.: 30

SEQ ID No.: 31

1512 CGG ATG GAA CTG AAC GGT GTG TAC GTG GAC ACA GAG TTC CTG AAG AAA CTC 1563  
 505 R M E L N G V Y V D T E F L K K L 521  
 3'CC CAT CTT GAC TTG CCA CAC ctt Cag cTG TcT 5'

<-----| TNELOW

"Sal I site "

ATHUP |----->  
 5' AAG Gtc Gac AGA GAT GCC CTC ATC CAA TAT ACC -3'  
 1387 ATG GAA AAA ACA GGA TTT AAG GTG GAT AGA GAT GCC CTC ATC CAA TAT ACC 1435  
 463 M E K T G F K V D R D A L I Q Y T 479

Figure 18/2:

SEQ ID No.: 32

SEQ ID No.: 33

SEQ ID No.: 22

```
2526   GGA CTG AAC TGG TAT GAG ACA AAA TAG           2553
843     G  L   N  W  Y  E  T  K  *
      3' TG ACC ATA CTC TGT TTT ATC ttcgaacgat 5'
      <-----| ATHLOW
```

Figure 19:

SEQ ID No.: 34

SEQ ID No.: 35

SEQ ID No.: 36

crossing point 2

```

chimera__8  IMEPLVSVLARMELNGVYVDTEFLKKLSEELYGKKLEELAEIYRIAGEPFNINSPKQVS|R
tne.rse_____IEMPLVSVLARMELNGVYVDTEFLKKLSEELYGKKLEELAEIYRIAGEPFNINSPKQVS|R
ath.rse_____IERPLIPVLYEMEKTGFKVDRDALIQYTKEIENKILKLETQIYQIAGEWFNINSPKQLS|R
  
```

A.

TNE polymerase nucleotide sequence 1642-1689

SEQ ID No.: 37

SEQ ID No.: 38

Bam HI site

```

          =====
1642  TCA CCG AAG CAG GTT TCA AGG ATC CTT TTT GAA AAA CTC GGC ATA AAA 1689
548   S  P  K  Q  V  S  R  I  L  F  E  K  L  G  I  K  563
  
```

SEQ ID No.: 39

SEQ ID No.: 40

SEQ ID No.: 41

SEQ ID No.: 42

ATH polymerase nucleotide sequence 1513 - 1560

```

1513  TCA CCG AAA CAG CTT TCT TAC ATT TTG TTT GAA AAG CTA AAA CTT CCT 1560
505   S  P  K  Q  L  S  Y  I  L  F  E  K  L  K  L  P  520
  
```

```

5'CA CCG AAA CAG CTT TCT agg atc cTG TTT GAA AAG CTA AAA CTT CCT G 3'
|-----m1----->
  
```

```

.....3'GT GGC TTT GTC GAA AGA tcc tag gAC AAA CTT TTC GAT TTT GAA GGA C 5'
<-----m2-----|
  
```

B.

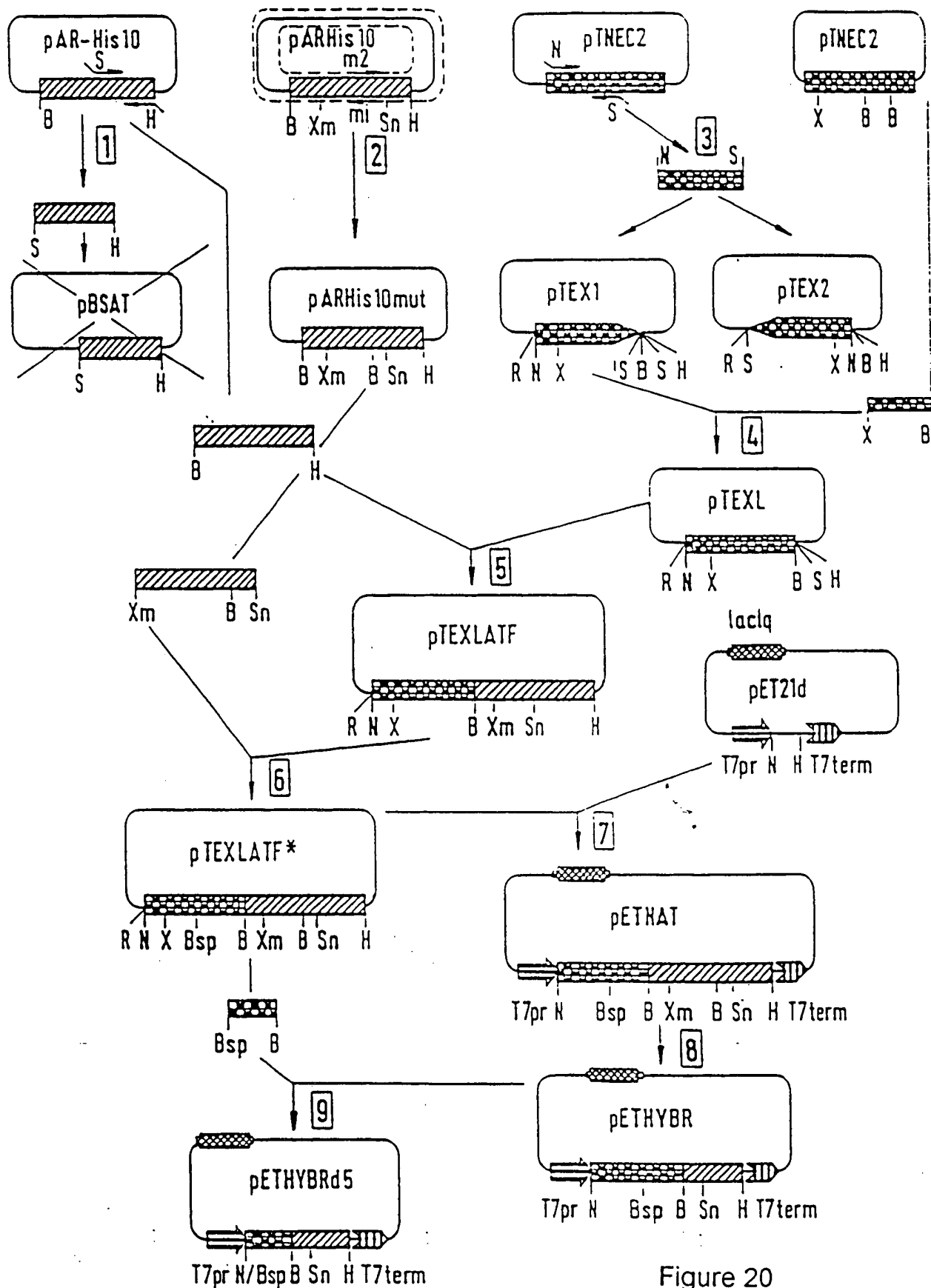


Figure 20

Figure 21:

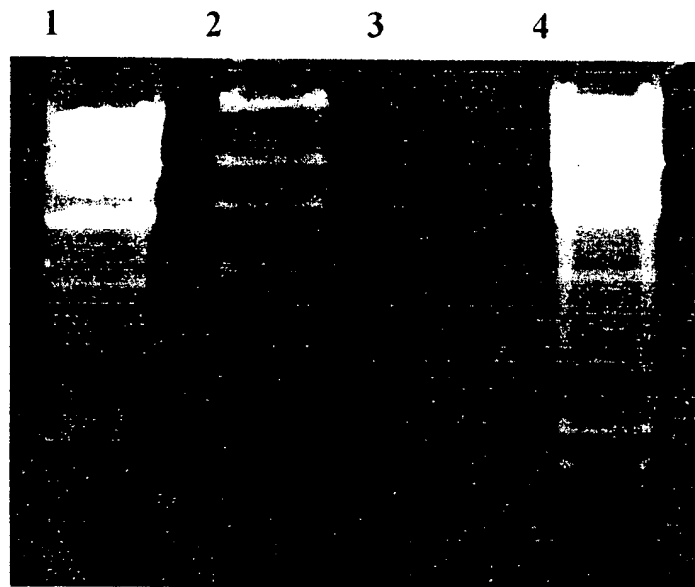


Figure 22:

Comparison of the reverse transcriptase activity of  
Tne/Ath hybrid polymerases with Tth- and C.therm.  
polymerase

